

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 20:25:53 ; Search time 77.81 Seconds

(without alignments)
254.443 Million cell updates/sec

Title: US-09-456-306-2

Perfect score: 2985

Sequence: 1 MAHSYAQLIDFLPAQGVKR.....GGVCAMIDLANSIRNIPFP 579

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36.*
1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseq/AA1981.DAT:*
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5: /cgn2_2/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseq/AA1986.DAT:*
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10: /cgn2_2/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseq/AA1990.DAT:*
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21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	560.5	18.8	592	9	P80477
2	537.5	18.0	570	11	R09316
3	530.5	17.8	570	11	R05793
4	522.5	17.5	562	14	W22459
5	517.5	17.3	562	9	P81153
6	515	17.3	548	18	W22460
7	514	17.2	548	17	R88842
8	514	17.2	548	18	R86881
9	514	17.2	548	18	W13731
10	496.5	16.6	669	13	R28618
11	495.5	16.6	669	13	R24798
12	495.5	16.6	669	13	R28617

13	495.5	16.6	669	13	R28623	Val571 deleted ace
14	495	16.6	666	13	R28616	Amino acids 650-65
15	494.5	16.6	669	13	R28624	Phe578 deleted ace
16	493.5	16.5	669	13	R28622	Asp376 deleted ace
17	493	16.5	669	13	R24800	Ser553 deleted ace
18	493	16.5	670	18	W22457	Arabidopsis wild-t
19	493	16.5	670	19	W59146	A. thaliana acetol
20	493	16.5	670	19	W59147	A. thaliana acetol
21	491.5	16.5	667	13	R28612	Amino acids 255-25
22	488.5	16.4	669	13	R28621	Met351 deleted ace
23	487.5	16.3	665	13	R28614	Amino acids 373-37
24	487.5	16.3	669	13	R28620	Lys256 deleted ace
25	487	16.3	660	13	R28615	Amino acids 569-57
26	486.5	16.3	669	13	R28619	Ala205 deleted ace
27	486	16.3	591	16	R87700	Streptococcus pneu
28	485	16.2	670	12	R11975	Tobacco herbicide-
29	485	16.2	670	13	R25913	ALS mutant of Arap
30	485	16.2	670	16	R63082	Herbicide-resistan
31	485	16.2	670	18	W22464	Arabidopsis herbic
32	484	16.2	664	13	R28613	Amino acids 348-35
33	482	16.1	666	13	R28609	Amino acids 119-12
34	478	16.0	577	17	W06554	R. capsulatus acet
35	475.5	15.9	668	13	R24801	Pro197/Ser653 dele
36	475.5	15.9	669	13	R24799	Pro197 deleted ace
37	473	15.8	666	13	R28610	Amino acids 194-19
38	461	15.4	594	15	R47188	Aceto-hydroxy acid
39	458	15.3	599	17	W16598	Corn acetoaldehyde
40	456	15.3	662	13	R28611	Amino acids 201-20
41	455	15.2	599	17	W16597	Corn acetoaldehyde
42	454	15.2	664	18	W22455	Tobacco wild-type
43	453	15.2	599	17	W03692	Corn acetoaldehyde
44	452	15.1	666	19	W79141	Plant acetoaldehyde
45	452	15.1	667	18	W22456	Tobacco wild-type

ALIGNMENTS

RESULT	ID	Standard: protein: 592 AA.
P80477		
AC	P80477;	
DT	06-NOV-1990 (first entry)	
DE	Pyruvate oxidase.	
KW	Pyruvate oxidase; ADP; ATP; pyruvic acid.	
PN	EP274425-A.	
PD	13-JUL-1988.	
PF	06-JAN-1988; 88EP-0300073.	
PR	15-MAY-1987; 87JP-0118161.	
PS	15-MAY-1987; 87JP-0000903.	
PA	(TOXN) TOYO JOZO KK.	
PI	Matsumura E, Imamura S, Sagai H, Misaki H, Nogota K;	
DR	WPI: 1988-192009/28.	
NR	N-PSDB; N81031.	
PT	Pyruvate oxidase prep. by recombinant DNA methods - used for	
PS	analysis of pyruvic acid, ADP, ATP or related non-phosphate cpds.	
CC	Disclosure; ; p: English.	
CC	This pyruvate oxidase has no Arpase contamination and can be used for	
CC	assaying ADP, ATP, pyruvic acid or other related non-phosphate cpds.	

Db 458 dflgvefndidfskldadyvmqatfrvnlkqldpvcfqakalaqhepvlldav 510

RESULT 3

ID R05793 standard; Protein: 570 AA.

XX R05793;

XX 15-FEB-1993 (first entry)

DE Pyruvate oxidase (wild-type).

XX POD; mutation; decarboxylation; assay.

XX Synthetic.

XX DE3833601-A.

XX 05-APR-1990.

XX 03-OCT-1988; 88DE-3833601.

XX 03-OCT-1988; 88DE-3833601.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Mollerling II, Schumacher G;

XX WPI; 1990-108586/15.

XX N-PSDB; Q03827.

XX New stable, mutated forms of pyruvate oxidase - having specific amino acid substitutions, useful as assay reagents, are encoded in new DNA

XX Claim 15; Page 6; 10pp; German.

XX The sequence of wild-type POD, given below, may be mutated so that at least 178-Pro and/or 425-Ala are exchanged.

XX The mutated pyruvate oxidase (POD) decarboxylates pyruvate with formation of H₂O₂ and is active without addn. of FAD, thiamine pyrophosphate and divalent metal ions. It is more stable (esp. in presence of salts and at alkaline pH) than wild-type enzyme, and is better suited for assay of pyruvate, or pyruvate-generating reactions.

XX See also Q08597.

XX Sequence 570 AA;

Query Match 17 88; Score 530.5; DB 11; Length 570;

Best Local Similarity 26.58; Pred. No. 3.9e-37;

Matches 141; Conservative 112; Mismatches 229; Indels 51; Gaps 9;

QY 9 LIOTLEAGVKKRIYGLGDSINPDAV--RQSDIEWVHVRNEEAFAGAESLITGEL 66

DB 17 vtlvleawgydhlylpggsinslmdlsnerdrlhyqyrtheevgamaaadaakltgk1 76

QY 67 AVCAASCCPCNTHLIGCLYDSHRNCAKVLAIASHIPSAOIGSTFFPQETHPBELFEKSCGY 136

DB 77 gvfgsaapggthlmnglydaredhylvalllgfgltgmndltfgemenpnyadvady 136

QY 127 CEVWNGEGGERLIHIAIOTSMAGKGVSVVIFGDIADKEDAGDGTYSNSTISSGTPVVF 186

DB 137 nvtavnaatclphvldaeitrayahgavavqldpvdipwqg-----lpaerpll-- 184

QY 187 DPTAALALVEAINNAKSVTLFCGAVNARAQVLELAEKIKSPIGHALGKQYIQHEHPNF 246

DB 185 -----yygigarkagkeltgskltklplmsyypakgyvadypa 224

QY 247 EVGMSGLGCGACVDASNEADLLILCTDPRYS--FLPKDNVAQVDINGAHIGRRTP 302

Db 225 ylganarvaqkpanaalagadvvlifvgunypfaevskafrntxyfjglddpaklgrkxh 284

QY 303 VKYPTGDVATIENTILPHVKEKTRDSFLDRLML--KAHERKLSVYETTHNNEKHPPI 359

DB 285 tdlavladagkflaallagvaresetpwwganlanvknwraylased-----kqegpl 338

QY 360 HPEYVASTILNELADKDAVFVDTGMCNWNHARYIENPEGTDFVGSFPHGTMANALPHAI 419

DB 339 qayqvlravnklaepdalysldygdlnnanrhklpcsrhlsnl-fatmgvgilpail 397

QY 420 GAQSVDRNRQVIAMCGDGLGMLLGLLTVKHLQPLKRAVENNSSLQMKVLEMLVEGQP 479

DB 398 aakinypergyfnlagdggasmtdlatqyghlpylnvfnvcygyfklkdegedtnqn 457

QY 480 EF-GTDHEEVNFAEIAAAGIKSVITDPKRVRE--QLAEALATPPGLIDIV 529

DB 458 dflgvefndidfskldadyvmqatfrvnlkqldpvcfqakalaqhepvlldav 510

RESULT 4

ID W22459 standard; Protein: 562 AA.

XX W22459;

XX 25-SEP-1997 (first entry)

DE E. coli acetylactate synthase isozyme I (sub-sequence E).

XX Acetylactate synthase; ALS; herbicide resistance; transgenic plant;

XX crop protection.

XX Escherichia coli.

XX US5605011-A.

XX 25-FEB-1997.

XX 26-AUG-1986; 86GUS-0900609.

XX 27-JUL-1987; 87IL-0083348.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PI Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;

PI Yadav NS;

XX WPI; 1997-153232/14.

PT Use of mutant acetylactate synthase genes - for transforming plants for resistance to sulphonylurea, triazopyrimidine sulphonamide and imidazolinone herbicides.

PT Claim 1; Fig 6a-f; 63pp; English.

XX Amino acid sub-sequences A-G respectively correspond to the large subunits of acetylactate synthase (ALS) isozymes I, II and III (W22459-61) from E. coli, and wild-type ALS proteins of yeast (W22458). Arabidopsis thaliana (W22457) and tobacco (W22455 and W22456). Comparison of these substantially conserved sequences with those of herbicide-resistant ALS enzymes (see also W22462-64) reveals the location of amino acid substns. that lead to herbicide resistance. In sub-sequence E, such a substn. is located at the gamma-1 position (any amino acid other than aspartic acid). A nucleic acid encoding an ALS from any source can be mutated so that the encoded enzyme contains this amino acid substn. Transformation of herbicide sensitive plants or plant cells with the nucleic acid results in resistance to the herbicide.

XX Sequence 562 AA;

Query Match 17.5%; Score 522.5; DB 18; Length 562;
 Best Local Similarity 28.1%; Pred. No. 1.9e-36;
 Matches 163; Conservative 107; Mismatches 239; Indels 71; Gaps 17;

QY 6 AEQIDTLEAGQVKRIYIGVDSLNPIDAVROS-DIEVHVHNEBAFAAGASLITG 64
 11 : 1111 :
 DB 16 aeflvhfliegqkivtgipgslipvdalsqstqirhlrlarhegagflagmarldg 75
 QY 65 ELAVCAASGPGENTHLLGCLYDSHRNGAKVLAIAHSIPSAQISFPQETHHELKES 124
 :
 DB 76 kpavmacsppgatlhlvaladarldslplcltqvpasmigtadqevdtygisipit 135
 QY 125 GYCEWVNGGEGERTLHNAIOSTMAGK-GVSVVVIPGDI-----AKEDAGDGT 171
 :
 DB 136 kmhlyvrhleeipqymsdfriagsrgpwwidipkdvqtavfeletcpmaekaaapa 195
 QY 172 YSNSTISSGTPVFPDPTEAALVEAINNASKSVTLFCGAVKNAQAULEAEKIKSPIG 231
 :
 DB 196 fseesi-----rdaam---lnaakrpvllyl99gvlnaparvrelaekaqplct 241
 QY 232 HALGKQVIOHNPFEVMSGLLGACVDASNEADLLILGTD-----PYSDFLPKD 285
 :
 DB 242 mtlmalgmipkaphlsiglmhgyrstnyllqeadllivlgartddraigtqecpna 301
 QY 286 NVAQVDINGAHIGRTTYKYP--VTGVAATIENTILPHVKEKTRSFDRMLKAHERK- 341
 :
 DB 302 klhvhldidraqgk---lkqphvalqadvddvlaqlipiv-eagpraehqjlvadlqref 357
 QY 342 ---LSSVETTYHNNEKHVPRIHEVYASILNELA---DKDAVFTVDTGCNWHARY--I 393
 :
 DB 358 pcpiipkacplsh-----yglinaaacvdnaalltcdvgqhgmtdaqaypl 404
 QY 394 ENPEGRDFVSGFRHGTMANALPHAIGASVDRNOVIAMCGDGIIMLIGELLTVKLIHQ 453
 :
 DB 405 nrp---rqlwtsgjgltmgfqlpaatgaalampdkvlfcsqdgslmmimgemataseng 461
 QY 454 LPLKAVFNNSSLGMV-KLEMLVEGQPEF-GTDHEEVNFAETIAAAGIKSVRIIDPKKVR 511
 :
 DB 462 ldvklllmneaiglvhqqgslyfegafvalcypgkinfmqiaagfgletcdlnneadpq 521
 QY 512 EQLAEALAPPGVLDIVDPNAL---SIPPTITWEQVWG 548
 :
 DB 522 aslqelilnrppallhvrldaekkyvmwppgaantemwg 561

RESULT 5
 P81153
 ID P81153 standard; protein: 562 AA.
 XX
 AC P81153;
 XX
 DT 17-OCT-1990 (first entry)
 XX
 DE Herbicide sensitive, wild type ALS.
 XX
 KW Tobacco; C3 mutant; SURA; acetolactase synthase; sulphonylurea herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP257993-A.
 XX
 PD 02-MAR-1988.
 XX
 PF 20-AUG-1987; 87BP-0307384.
 XX
 PR 26-AUG-1986; 86US-0900609.
 XX
 XX (DUPO) DU PONT DE NEMOURS CO.
 XX
 PA Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Yadav NS;
 XX
 DR WPI; 1988-058164/09.
 XX

PT New nucleic acid fragment coding - for mutant aceto-lactate
 PT synthetase resistant to sulphonyl-urea herbicides, and
 PT transformed resistant crop plants.
 PS Disclosure; P; English.
 XX
 XX
 CC The sequence is that of the wild type herbicide sensitive form of ALS
 CC encoded by the SURA gene.
 CC See also P81149-55.
 XX
 SQ Sequence 562 AA;

Query Match 17.3%; Score 517.5; DB 9; Length 562;
 Best Local Similarity 27.9%; Pred. No. 5e-36;
 Matches 162; Conservative 107; Mismatches 240; Indels 71; Gaps 17;

QY 6 AEQIDTLEAGQVKRIYIGVDSLNPIDAVROS-DIEVHVHNEBAFAAGASLITG 64
 11 : 1111 :
 DB 16 aeflvhfliegqkivtgipgslipvdalsqstqirhlrlarhegagflagmarldg 75
 QY 65 ELAVCAASGPGENTHLLGCLYDSHRNGAKVLAIAHSIPSAQISFPQETHHELKES 124
 :
 DB 76 kpavmacsppgatlhlvaladarldslplcltqvpasmigtadqevdtygisipit 135
 QY 125 GYCEWVNGGEGERTLHNAIOSTMAGK-GVSVVVIPGDI-----AKEDAGDGT 171
 :
 DB 136 kmhlyvrhleeipqymsdfriagsrgpwwidipkdvqtavfeletcpmaekaaapa 195
 QY 172 YSNSTISSGTPVFPDPTEAALVEAINNASKSVTLFCGAVKNAQAULEAEKIKSPIG 231
 :
 DB 196 fseesi-----rdaam---lnaakrpvllyl99gvlnaparvrelaekaqplct 241
 QY 232 HALGKQVIOHNPFEVMSGLLGACVDASNEADLLILGTD-----PYSDFLPKD 285
 :
 DB 242 mtlmalgmipkaphlsiglmhgyrstnyllqeadllivlgartddraigtqecpna 301
 QY 286 NVAQVDINGAHIGRTTYKYP--VTGVAATIENTILPHVKEKTRSFDRMLKAHERK- 341
 :
 DB 302 klhvhldidraqgk---lkqphvalqadvddvlaqlipiv-eagpraehqjlvadlqref 357
 QY 342 ---LSSVETTYHNNEKHVPRIHEVYASILNELA---DKDAVFTVDTGCNWHARY--I 393
 :
 DB 358 pcpiipkacplsh-----yglinaaacvdnaalltcdvgqhgmtdaqaypl 404
 QY 394 ENPEGRDFVSGFRHGTMANALPHAIGASVDRNOVIAMCGDGIIMLIGELLTVKLIHQ 453
 :
 DB 405 nrp---rqlwtsgjgltmgfqlpaatgaalampdkvlfcsqdgslmmimgemataseng 461
 QY 454 LPLKAVFNNSSLGMV-KLEMLVEGQPEF-GTDHEEVNFAETIAAAGIKSVRIIDPKKVR 511
 :
 DB 462 ldvklllmneaiglvhqqgslyfegafvalcypgkinfmqiaagfgletcdlnneadpq 521
 QY 512 EQLAEALAPPGVLDIVDPNAL---SIPPTITWEQVWG 548
 :
 DB 522 aslqelilnrppallhvrldaekkyvmwppgaantemwg 561

RESULT 6
 W22460
 ID W22460 standard; Protein: 548 AA.
 XX
 AC W22460;
 XX
 DT 25-SEP-1997 (first entry)
 XX
 DE E. coli acetolactate synthase isozyme II (sub-sequence F).
 XX
 KW Acetolactate synthase; ALS; herbicide resistance; transgenic plant;
 XX
 OS Escherichia coli.
 XX


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OY 66 LAVCAASGPGNTLHIOGLYDSHRNGAKVLAISHIPSAOIGSTFFOETHPEILFEKCSG 125
DB 64 tgvciatspgpatnlitgladallidsipvaltgvsapflgtdafgvdvlgslactk 123
OY 126 YCEWNGGEOGERILHHAIOSTMACK-GVSVVVIRPGDIADAGDGTSSNSTISSGTPV 184
DB 124 hsfllvqslleelprlmaaeafdvacsgrppvldipkdi-qlasgdlpewftven--evt 180
OY 185 FPDPEAAALVEAINNASKSVTLFCGAGVKNARA--QVLELAEKIKSPIGHALGKQYIOH 242
DB 181 fph-aevqarqmlakqdkpmllyvgvgmagavpalreflaatkmpatcltklgavea 239
OY 243 ENPEVSGSLGLGACVDASNEADLLILGTDF-----PYSDFLPKDNVAQVDINGAH 296
DB 240 dypyllygmlymgtkaanfavecdlllavgarfdadrvtgkintfaphasvilmidpae 299
OY 297 IGRRTTVKPYPTGVAATIENTILPHVKEKTRSFIDRLMLKAHERKLSVETTYTHNVEKH 356
DB 300 mklrqahvalqgdlnalipalqplngcdwqghcaqlrdenswr-----ydh----- 347
OY 357 VPIHEVYASINELADK---DAVFTVDTGMCNVWHARIEN--PEGTRDFVGSRRHGTM 411
DB 348 -pgdaiyaplllkqlstckpadcvtldvgqghmaaqhiahtrpe---nfltsqglgtm 403
OY 412 ANALPHAIGAOSVDRNRROYIAMCGDGLGMLGELLTYKHLQPLKAVFNNSSIGMYKL 471
DB 404 gfglpaaavayarpndvvcisgdsfmmnvqelgtvkrkqplkivlldnqrlgmvrq 463
OY 472 EMLVEGQPEFG---TDHEEVNFAEIAAAGIKSVRITDPKKVROLAALAYPGPVLID 527
DB 464 wqglffqysetcltldnpd--flmlasafghghitrkdqveaaltdmlnsdpyllh 521
OY 528 IYTD 531
DB 522 vsid 525

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RESULT 8
R86881
ID R86881 standard; Protein: 548 AA.

XX R86881:
XX 15-OCT-1995 (first entry)
XX DE E. coli threonine-deaminase.
XX KW thrABC operon; ilvGMDA operon; thrA gene; ilvA gene; amino acid;
XX aspartokinase-I; homoserine-dehydrogenase-I; threonine-deaminase;
XX enzyme; metabolic engineering; L-isoleucine; feedback-inhibition.
XX OS Escherichia coli.
XX PN EP68555-A1.
XX PD 06-DEC-1995.
XX PE 30-MAY-1995; 95EP-0108315.
XX PR 30-MAY-1994; 94JP-0116340.
XX PA (AJIN) AJINOMOTO CO INC.
XX PI Hashiguchi K, Kishino H, Matsui H, Tsujimoto N;
XX DR WPI: 1996-012380/02.
XX N-PSDB: T07115.
XX PT New Escherichia transformant producing L-isoleucine - carrying thr
XX ABC operon, ilv GMDA operon and opt. lys C gene, all of which are
XX released from feedback inhibition

PS Disclosure; Page 35-38; 48pp; English.
XX CC This sequence is encoded by an E. coli ilvGMDA operon which comprises
CC a ilvA gene coding for threonine-deaminase. This enzyme is released
CC from inhibition by L-isoleucine, during fermentation of E. coli for
CC the production of L-isoleucine.
XX Sequence 548 AA;

Query Match 17.2%; Score 514; DB 17; Length 548;
Best Local Similarity 30.1%; Pred. No. 9.6e-36;
Matches 164; Conservative 91; Mismatches 249; Indels 40; Gaps 13;

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OY 6 AEQLDITLEAGCKRIYGLVYDSLRNPYDAVARQSDIEVWHVNRNEEAAFAAGASLTGE 65
DB 4 agwvvalraqvntvtrfyppgaipmyvdalyydgvehltrcheggaamaigyaratgk 63
OY 66 LAVCAASGPGNTLHIOGLYDSHRNGAKVLAISHIPSAOIGSTFFOETHPEILFEKCSG 125
DB 64 tgvciatspgpatnlitgladallidsipvaltgvsapflgtdafgvdvlgslactk 123
OY 126 YCEWNGGEOGERILHHAIOSTMACK-GVSVVVIRPGDIADAGDGTSSNSTISSGTPV 184
DB 124 hsfllvqslleelprlmaaeafdvacsgrppvldipkdi-qlasgdlpewftven--evt 180
OY 185 FPDPEAAALVEAINNASKSVTLFCGAGVKNARA--QVLELAEKIKSPIGHALGKQYIOH 242
DB 181 fph-aevqarqmlakqdkpmllyvgvgmagavpalreflaatkmpatcltklgavea 239
OY 243 ENPEVSGSLGLGACVDASNEADLLILGTDF-----PYSDFLPKDNVAQVDINGAH 296
DB 240 dypyllygmlymgtkaanfavecdlllavgarfdadrvtgkintfaphasvilmidpae 299
OY 297 IGRRTTVKPYPTGVAATIENTILPHVKEKTRSFIDRLMLKAHERKLSVETTYTHNVEKH 356
DB 300 mklrqahvalqgdlnalipalqplngcdwqghcaqlrdenswr-----ydh----- 347
OY 357 VPIHEVYASINELADK---DAVFTVDTGMCNVWHARIEN--PEGTRDFVGSRRHGTM 411
DB 348 -pgdaiyaplllkqlstckpadcvtldvgqghmaaqhiahtrpe---nfltsqglgtm 403
OY 412 ANALPHAIGAOSVDRNRROYIAMCGDGLGMLGELLTYKHLQPLKAVFNNSSIGMYKL 471
DB 404 gfglpaaavayarpndvvcisgdsfmmnvqelgtvkrkqplkivlldnqrlgmvrq 463
OY 472 EMLVEGQPEFG---TDHEEVNFAEIAAAGIKSVRITDPKKVROLAALAYPGPVLID 527
DB 464 wqglffqysetcltldnpd--flmlasafghghitrkdqveaaltdmlnsdpyllh 521
OY 528 IYTD 531
DB 522 vsid 525

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RESULT 9
W13731
ID W13731 standard; Protein: 548 AA.
XX W13731:
XX 24-NOV-1997 (first entry)
XX DE Protein product of Escherichia coli ilvG gene open reading frame 2.
XX KW ilvG; L-isoleucine; production; open reading frame 2; ORF2.
XX OS Escherichia coli.
XX PN WO9708333-A1.
XX PD 06-MAR-1997.


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Db 446 qkqkfpIsftfgeaippqyaikvIdeltdgkaIstvgvghqmwaaqfy-nykkrpqrwl 504
QY 404 GSFRRGTMANALPHATIGASVDRNRQVIAMCGDGLGMLLGLTLTKLHQLPLKAVFNN 463
Db 505 ssqgIlgamvfgIpaalgasvampdaIvdlgdgsfImmvgeIatIvenIpkvIllnn 564
QY 464 SSIGAWKLEMLVE-----GOPEFGTDHEEV--NFAETIAAAGIKSVRTDPK 508
Db 565 qhlgmv-----mqwedrfykanrahtfIgdP---aqedeIpfmllIfaacgIpaarvtkka 618
QY 509 KYREQALAEALAYPGVYLIDITDPNALSIPTPI 541
Db 619 dIreaIqmltdfppylIdvIc-phqehvIpmI 650

RESULT 11
R24798 ID R24798 standard; Protein: 669 AA.
AC R24798;
XX
XX 11-DEC-1992 (first entry)
XX
XX Trp574 deleted acetohydroxy acid synthase.
DE
XX
XX AHAS: herbicide resistance; plants; imidazolinones;
KW triazolopyrimidines; sulphonylureas.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP492113-A.
XX
XX 01-JUL-1992.
XX
XX 12-NOV-1991; 91EP-0119254.
XX
XX 27-DEC-1990; 90US-0633210.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
PA
XX
XX Chaleff RS, Hand JM, Singh BK;
XX
XX WPI: 1992-218438/27.
XX
XX N-PSDB: Q26001.
XX
XX Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT nucleic acid sequences which can confer herbicide resistance to
PT plants
XX
XX Example: Page 8; 37pp; English.
XX
XX The sequence is that of Trp574 deleted acetohydroxy acid synthase
CC (AHAS) which is herbicide resistant. Transgenic plants may be
CC produced which contain the modified gene and produce the Trp574
CC deleted AHAS in the presence of an inhibitory amt. of herbicide.
CC The gene can thus be used to provide crop plants with resistance
CC to herbicides such as imidazolinones, triazolopyrimidines and
CC sulphonylureas. See also R24797 and R24801.
XX
XX
XX Sequence 669 AA:
SQ

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Query Match 16.6%; Score 495.5; DB 13; Length 669;
Best Local Similarity 27.5%; Pred. No. 5,1e-34;
Matches 157; Conservative 97; Mismatches 263; Indels 53; Gaps 13;

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QY 6 AEOIDTLEAGVKRIYGLVGSLSNPIDAV-RQSDIENVHVRNEPAAPAGAESLTIG 64
Db 100 adIvleaIerqvetvfaypggsmeIhgaItrssIrIrvIprheggvfaeagYarssg 159
QY 65 ELAVCAASGPGNTHLIOGLYDSHRNGAKVLAISHIPSAOIGSTPFQETHPEILFKES 124
Db 160 kpqIcIatsgppatIvsgIadallIsvpIvaItvgvPrImIgtIdafqetpIveItrst 219

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QY 125 GYCEWNGGEGEERILHHAIOSTMAGK-GVSEVVYIPGDIKEDAGDGYTSNSTISGTPV 183
Db 220 khnyIvmvedIprIleaefIatsgrpypvIvdpkdl-qgqIaIpmwegaamlIpyms 278
QY 184 VEPDPTFAAL--VEAINNAKSVTLFCGAGVKNAKRAOVLEAEIKSPIGHALGKOYT 240
Db 279 rmpkPedsIhIeqIvrlIseskKpvlYvggclssdelgrfvelIgtIvpaStImglgsy 338
QY 241 QHENFEVGMGSLGCGACVQASNEADLLILGDFE-----PYSDFLPKNNVQAVDING 294
Db 339 pcddeIsIhmIgmhgtvYanyavehsdlIafgyrIddrvtqkIleaIstrakIvIdIdS 398
QY 295 AHIGRTTVKYPVTDDVATIENTILPHVKERTDRSEFLDRL--KAHERKLSVVEYETHN 352
Db 399 aeIqknktpIhsvsgdvkIalIq-----mmkvIenraeeIkIdfgyvrneIn 445
QY 353 VEKH-----VPIHEVYASILNELADKDAVFTYDTGKCNNVHARITENPEGTDF 402
Db 446 vqkqkfpIsftfgeaippqyaikvIdeltdgkaIstvgvghqmwaaqfy-nykkrpqrw 504
QY 403 VGSFRRGTMANALPHATIGASVDRNRQVIAMCGDGLGMLLGLTLTKLHQLPLKAVEN 462
Db 505 IassgIlgamvfgIpaalgasvampdaIvdlgdgsfImmvgeIatIvenIpkvIllnn 564
QY 463 NSSIGMWKLE-----MLVEGQPEFGTDHEEV--NFAETIAAAGIKSVRTDPKVR 511
Db 565 nqhIgmwgedrfykanrahtfIgdP---aqedeIpfmllIfaacgIpaarIltkadI 621
QY 512 EQALAEALAYPGVYLIDITDPNALSIPTPI 541
Db 622 eaIqcmItdfppylIdvIc-phqehvIpmI 650

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RESULT 12
R28617 ID R28617 standard; Protein: 669 AA.
XX
XX R28617;
XX
XX 11-DEC-1992 (first entry)
XX
XX Gly121 deleted acetohydroxy acid synthase.
DE
XX
XX AHAS: herbicide resistance; plants; imidazolinones;
KW triazolopyrimidines; sulphonylureas.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP492113-A.
XX
XX 01-JUL-1992.
XX
XX 12-NOV-1991; 91EP-0119254.
XX
XX 27-DEC-1990; 90US-0633210.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
PA
XX
XX Chaleff RS, Hand JM, Singh BK;
XX
XX WPI: 1992-218438/27.
XX
XX Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT nucleic acid sequences which can confer herbicide resistance to
PT plants
XX
XX Claim 4; Page 20; 37pp; English.
XX
XX The sequence is that of Gly121 deleted acetohydroxy acid synthase
CC (AHAS) which is herbicide resistant. Transgenic plants may be
CC produced which contain the modified gene and produce the Gly121
CC deleted AHAS in the presence of an inhibitory amt. of herbicide.
CC

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XX AC R28616;
XX AC 11-DEC-1992 (first entry)
XX DF
XX DE Amino acids 650-653 deleted acetohydroxy acid synthase.
XX KM AHAAS; herbicide resistance; plants; imidazolinones;
XX KM triazolopyrimidines; sulphonylureas.
XX OS Arabidopsis thaliana.
XX PN EP492113-A.
XX PD 01-JUL-1992.
XX PF 12-NOV-1991; 91EP-0119254.
XX PR 27-DEC-1990; 90US-0633210.
XX PA (AMCY ) AMERICAN CYANAMID CO.
XX PI Chaleff RS, Hand JM, Singh BK;
XX DR WPI; 1992-218438/27.
XX ACeto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT nucleic acid sequences which can confer herbicide resistance to
PT plants
XX PS Claim 3; Page 20; 37pp; English.
XX CC The sequence is that of amino acids 650-653 deleted acetohydroxy acid
XX CC synthase (AHAAS) which is herbicide resistant. Transgenic plants may be
XX CC produced which contain the modified gene and produce the 650-653
XX CC deleted AHAAS in the presence of an inhibitory amt. of herbicide.
XX CC The gene can thus be used to provide crop plants with resistance
XX CC to herbicides such as imidazolinones, triazolopyrimidines and
XX CC sulphonylureas. See also R24798-R24801 and R28609-R28624.
XX SQ Sequence 666 AA;

Query Match 16.6%; Score 495; DB 13; Length 666;
Best Local Similarity 27.4%; Pred. No. 5.6e-34;
Matches 159; Conservative 99; Mismatches 262; Indels 60; Gaps 14;

QY 6 AEQLIDTLEAGCVKRTYGLVGSNLPIYDAV-RQSDIEVHVHNEEAAFAAGASLITG 64
DB 100 adlvealerqgvelfaypggasmelhgaltlrsslrnviprhqggvfaaeyarssg 159
QY 65 ELAVCAASGPGENTLIGLVDSHNGAKVLAIAHSIPSAOIGSNFPOFTHPEILFEKES 124
DB 160 kpgciatspgpatnlvsgladallidsvplaitqgvprimgitafqetpivertrsit 219
QY 125 GYCEWVNGCEGDERILHHAIOSTMAGK-GVSVVVPIGDIKADAGDGYVSNSTISSGTPV 183
DB 220 khnylvmvdvedprilaeafatsegrpqlvdvdkd-qgqlaipmweqamrlpygms 278
QY 184 VPPDPTTEAAL--VEAINNAKSVTLPGCAGYKNAKRAOVLEIAEKIKSIGALGKQYI 240
DB 279 rmpkprpeshleglvrlliseskprlyvggcinsdelqfgrfveltgjlvastlmglsy 338
QY 241 QHENFEFVGMSGLLGAGCVDASNEADLILIGTDF-----PYSDFLPKDNVAQVDING 294
DB 339 pcdelslhmimgtvyanyavehsdlilaftgrfdtdvsgklaefstakivhidids 398
QY 295 AHIGRRTVKYPVGDVAATTENILPHVKEKTRDSFLDRLM--KAHERKLSSVETTYHN 352
DB 399 aelgknkphvsvsgdvklalqg-----mmkvlenreeelklldgvrnnein 445
QY 353 VEKH-----VPIHPEVASILNELADKDAVFTVDTGCNWHARYIENPGTRDF 402

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DB 446 vqgkfpisfktfgaelpgyalkvldeltdgkalisctvgvghmwaqfy-nykkprgw 504
QY 403 VGSFRHGTMANALPHAIGASVDRNROYIAMCGDGLGMLGELLTVKHLHPLKAVVEN 462
DB 505 lssgglgmgfslpaaisvaanpdaivddgdsfflmvgetatirvenlpkvklln 564
QY 463 NSSLIGMKVLEMLVE-----GQPEFGTDHERV--NFAETIAAAGIKSVRTDP 507
DB 565 nqlhgmv---nqwedrifykanrahtflgdp---aqedelfpmliffaacsqpaarvck 618
QY 508 KKVREQLAEALAYRGPVLDIYTDENALSIPTTWEDQM 547
DB 619 adlreaigtmdtpgylldvic-phgehvlpyglfndvl 657

RESULT 15
R28624
ID R28624 standard; Protein; 669 AA.
XX AC R28624;
XX DF 11-DEC-1992 (first entry)
XX DE Phe578 deleted acetohydroxy acid synthase.
XX KM AHAAS; herbicide resistance; plants; imidazolinones;
XX KM triazolopyrimidines; sulphonylureas.
XX OS Arabidopsis thaliana.
XX PN EP492113-A.
XX PD 01-JUL-1992.
XX PF 12-NOV-1991; 91EP-0119254.
XX PR 27-DEC-1990; 90US-0633210.
XX PA (AMCY ) AMERICAN CYANAMID CO.
XX PI Chaleff RS, Hand JM, Singh BK;
XX DR WPI; 1992-218438/27.
XX ACeto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT nucleic acid sequences which can confer herbicide resistance to
PT plants
XX PS Claim 4; Page 20; 37pp; English.
XX CC The sequence is that of Phe578 deleted acetohydroxy acid synthase
XX CC (AHAAS) which is herbicide resistant. Transgenic plants may be
XX CC produced which contain the modified gene and produce the Phe578
XX CC deleted AHAAS in the presence of an inhibitory amt. of herbicide.
XX CC The gene can thus be used to provide crop plants with resistance
XX CC to herbicides such as imidazolinones, triazolopyrimidines and
XX CC sulphonylureas. See also R24798-R24801 and R28609-R28623.
XX SQ Sequence 669 AA;

Query Match 16.6%; Score 494.5; DB 13; Length 669;
Best Local Similarity 27.5%; Pred. No. 6.2e-34;
Matches 157; Conservative 99; Mismatches 261; Indels 53; Gaps 13;

QY 6 AEQLIDTLEAGCVKRTYGLVGSNLPIYDAV-RQSDIEVHVHNEEAAFAAGASLITG 64
DB 100 adlvealerqgvelfaypggasmelhgaltlrsslrnviprhqggvfaaeyarssg 159
QY 65 ELAVCAASGPGENTLIGLVDSHNGAKVLAIAHSIPSAOIGSNFPOFTHPEILFEKES 124
DB 160 kpgciatspgpatnlvsgladallidsvplaitqgvprimgitafqetpivertrsit 219

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